SEQUENCE LISTING


<110> Glaxo Group Limited
Farrow, Stuart N
Kaptein, Allard
Kitson, Jeremy DA
Winder, Alison J

<120> Novel Ligand

<130> PG3600

<140> PCT/EP99/07303
<141> 1999-10-05

<150> GB 9828628.9
<151> 1998-12-23

<160> 8

<170> PatentIn Ver. 2.1

<210> 1
<211> 153
<212> PRT
<213> Homo sapiens

<400> 1

```
Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln Asp Cys Leu Gln
  1               5                  10                  15

Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser Tyr Thr
            20                  25                  30

Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu Glu
        35                  40                  45

Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile Tyr
    50                  55                  60

Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu Ile
65                  70                  75                  80

Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr
                85                  90                  95

Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn Ser
            100                 105                 110

Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Gly Leu Gln
        115                 120                 125

Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp Val
    130                 135                 140

Thr Phe Phe Gly Ala Leu Lys Leu Leu
145                 150
```

<210> 2
<211> 285
<212> PRT
<213> Homo sapiens

<400> 2
Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu
1 5 10 15

Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
20 25 30

Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
35 40 45

Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
50 55 60

Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
65 70 75 80

Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
85 90 95

Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
100 105 110

Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
115 120 125

Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
130 135 140

Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
145 150 155 160

Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
165 170 175

Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
180 185 190

Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
195 200 205

Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
210 215 220

Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
225 230 235 240

Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
245 250 255

Asp Gly Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu
260 265 270

Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
275 280 285

<210> 3
<211> 462
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(462)

<400> 3
```
cgt gcc gtt cag ggt cca gaa gaa aca gtc act caa gac tgc ttg caa   48
Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln Asp Cys Leu Gln
  1               5                  10                  15

ctg att gca gac agt gaa aca cca act ata caa aaa gga tct tac aca   96
Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser Tyr Thr
            20                  25                  30

ttt gtt cca tgg ctt ctc agc ttt aaa agg gga agt gcc cta gaa gaa   144
Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu Glu
        35                  40                  45

aaa gag aat aaa ata ttg gtc aaa gaa act ggt tac ttt ttt ata tat   192
Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile Tyr
    50                  55                  60

ggt cag gtt tta tat act gat aag acc tac gcc atg gga cat cta att   240
Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu Ile
65                  70                  75                  80

cag agg aag aag gtc cat gtc ttt ggg gat gaa ttg agt ctg gtg act   288
Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr
                85                  90                  95

ttg ttt cga tgt att caa aat atg cct gaa aca cta ccc aat aat tcc   336
Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn Ser
            100                 105                 110

tgc tat tca gct ggc att gca aaa ctg gaa gaa gga gat gga ctc caa   384
Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Gly Leu Gln
        115                 120                 125

ctt gca ata cca aga gaa aat gca caa ata tca ctg gat gga gat gtc   432
Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp Val
    130                 135                 140

aca ttt ttt ggt gca ttg aaa ctg ctg tga                          462
Thr Phe Phe Gly Ala Leu Lys Leu Leu
145                 150
```

<210> 4
<211> 858
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(858)

<400> 4
```
atg gat gac tcc aca gaa agg gag cag tca cgc ctt act tct tgc ctt   48
Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu
  1               5                  10                  15

aag aaa aga gaa gaa atg aaa ctg aag gag tgt gtt tcc atc ctc cca   96
Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
```

```
                20                  25                  30

cgg aag gaa agc ccc tct gtc cga tcc tcc aaa gac gga aag ctg ctg   144
Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
            35                  40                  45

gct gca acc ttg ctg ctg gca ctg ctg tct tgc tgc ctc acg gtg gtg   192
Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
        50                  55                  60

tct ttc tac cag gtg gcc gcc ctg caa ggg gac ctg gcc agc ctc cgg   240
Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
    65                  70                  75                  80

gca gag ctg cag ggc cac cac gcg gag aag ctg cca gca gga gca gga   288
Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
                85                  90                  95

gcc ccc aag gcc ggc ctg gag gaa gct cca gct gtc acc gcg gga ctg   336
Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
            100                 105                 110

aaa atc ttt gaa cca cca gct cca gga gaa ggc aac tcc agt cag aac   384
Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
        115                 120                 125

agc aga aat aag cgt gcc gtt cag ggt cca gaa gaa aca gtc act caa   432
Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
    130                 135                 140

gac tgc ttg caa ctg att gca gac agt gaa aca cca act ata caa aaa   480
Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
145                 150                 155                 160

gga tct tac aca ttt gtt cca tgg ctt ctc agc ttt aaa agg gga agt   528
Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
                165                 170                 175

gcc cta gaa gaa aaa gag aat aaa ata ttg gtc aaa gaa act ggt tac   576
Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
            180                 185                 190

ttt ttt ata tat ggt cag gtt tta tat act gat aag acc tac gcc atg   624
Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
        195                 200                 205

gga cat cta att cag agg aag aag gtc cat gtc ttt ggg gat gaa ttg   672
Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
    210                 215                 220

agt ctg gtg act ttg ttt cga tgt att caa aat atg cct gaa aca cta   720
Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
225                 230                 235                 240

ccc aat aat tcc tgc tat tca gct ggc att gca aaa ctg gaa gaa gga   768
Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
                245                 250                 255

gat gga ctc caa ctt gca ata cca aga gaa aat gca caa ata tca ctg   816
Asp Gly Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu
            260                 265                 270

gat gga gat gtc aca ttt ttt ggt gca ttg aaa ctg ctg tga           858
```

```
Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
        275                 280                 285
```

<210> 5
<211> 144
<212> PRT
<213> Mus sp.

<400> 5

```
Ile Ile Gln Asp Cys Leu Gln Leu Ile Ala Asp Ser Asp Thr Pro Thr
  1               5                  10                  15

Ile Arg Lys Gly Thr Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys
            20                  25                  30

Arg Gly Asn Ala Leu Glu Glu Lys Glu Asn Lys Ile Val Val Arg Gln
        35                  40                  45

Thr Gly Tyr Phe Phe Ile Tyr Ser Gln Val Leu Tyr Thr Asp Pro Ile
    50                  55                  60

Phe Ala Met Gly His Val Ile Gln Arg Lys Lys Val His Val Phe Gly
65                  70                  75                  80

Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro
                85                  90                  95

Lys Thr Leu Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Arg Leu
            100                 105                 110

Glu Glu Gly Asp Glu Ile Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln
        115                 120                 125

Ile Ser Arg Asn Gly Asp Asp Thr Phe Phe Gly Ala Leu Lys Leu Leu
    130                 135                 140
```

<210> 6
<211> 309
<212> PRT
<213> Mus sp.

<400> 6

```
Met Asp Glu Ser Ala Lys Thr Leu Pro Pro Pro Cys Leu Cys Phe Cys
  1               5                  10                  15

Ser Glu Lys Gly Glu Asp Met Lys Val Gly Tyr Asp Pro Ile Thr Pro
            20                  25                  30

Gln Lys Glu Glu Gly Ala Trp Phe Gly Ile Cys Arg Asp Gly Arg Leu
        35                  40                  45

Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Ser Ser Phe Thr Ala
    50                  55                  60

Met Ser Leu Tyr Gln Leu Ala Ala Leu Gln Ala Asp Leu Met Asn Leu
65                  70                  75                  80

Arg Met Glu Leu Gln Ser Tyr Arg Gly Ser Ala Thr Pro Ala Ala Ala
```

```
                85                  90                  95

Gly Ala Pro Glu Leu Thr Ala Gly Val Lys Leu Leu Thr Pro Ala Ala
            100                 105                 110

Pro Arg Pro His Asn Ser Ser Arg Gly His Arg Asn Arg Arg Ala Phe
        115                 120                 125

Gln Gly Pro Glu Glu Thr Glu Gln Asp Val Asp Leu Ser Ala Pro Pro
    130                 135                 140

Ala Pro Cys Leu Pro Gly Cys Arg His Ser Gln His Asp Asp Asn Gly
145                 150                 155                 160

Met Asn Leu Arg Asn Ile Ile Gln Asp Cys Leu Gln Leu Ile Ala Asp
                165                 170                 175

Ser Asp Thr Pro Thr Ile Arg Lys Gly Thr Tyr Thr Phe Val Pro Trp
            180                 185                 190

Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu Glu Glu Lys Glu Asn Lys
        195                 200                 205

Ile Val Val Arg Gln Thr Gly Tyr Phe Phe Ile Tyr Ser Gln Val Leu
    210                 215                 220

Tyr Thr Asp Pro Ile Phe Ala Met Gly His Val Ile Gln Arg Lys Lys
225                 230                 235                 240

Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys
                245                 250                 255

Ile Gln Asn Met Pro Lys Thr Leu Pro Asn Asn Ser Cys Tyr Ser Ala
            260                 265                 270

Gly Ile Ala Arg Leu Glu Glu Gly Asp Glu Ile Gln Leu Ala Ile Pro
        275                 280                 285

Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly Asp Asp Thr Phe Phe Gly
    290                 295                 300

Ala Leu Lys Leu Leu
305


<210> 7
<211> 435
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(435)

<400> 7
atc att caa gac tgt ctg cag ctg att gca gac agc gac acg ccg act   48
Ile Ile Gln Asp Cys Leu Gln Leu Ile Ala Asp Ser Asp Thr Pro Thr
  1               5                  10                  15

ata cga aaa gga act tac aca ttt gtt cca tgg ctt ctc agc ttt aaa   96
Ile Arg Lys Gly Thr Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys
            20                  25                  30
```

```
aga gga aat gcc ttg gag gag aaa gag aac aaa ata gtg gtg agg caa   144
Arg Gly Asn Ala Leu Glu Glu Lys Glu Asn Lys Ile Val Val Arg Gln
          35                  40                  45

aca ggc tat ttc ttc atc tac agc cag gtt cta tac acg gac ccc atc   192
Thr Gly Tyr Phe Phe Ile Tyr Ser Gln Val Leu Tyr Thr Asp Pro Ile
      50                  55                  60

ttt gct atg ggt cat gtc atc cag agg aag aaa gta cac gtc ttt ggg   240
Phe Ala Met Gly His Val Ile Gln Arg Lys Lys Val His Val Phe Gly
 65                  70                  75                  80

gac gag ctg agc ctg gtg acc ctg ttc cga tgt att cag aat atg ccc   288
Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro
                85                  90                  95

aaa aca ctg ccc aac aat tcc tgc tac tcg gct ggc atc gcg agg ctg   336
Lys Thr Leu Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Arg Leu
            100                 105                 110

gaa gaa gga gat gag att cag ctt gca att cct cgg gag aat gca cag   384
Glu Glu Gly Asp Glu Ile Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln
        115                 120                 125

att tca cgc aac gga gac gac acc ttc ttt ggt gcc cta aaa ctg ctg   432
Ile Ser Arg Asn Gly Asp Asp Thr Phe Phe Gly Ala Leu Lys Leu Leu
    130                 135                 140

taa                                                               435
```

<210> 8
<211> 930
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(930)

<400> 8

```
atg gat gag tct gca aag acc ctg cca cca ccg tgc ctc tgt ttt tgc   48
Met Asp Glu Ser Ala Lys Thr Leu Pro Pro Pro Cys Leu Cys Phe Cys
  1               5                  10                  15

tcc gag aaa gga gaa gat atg aaa gtg gga tat gat ccc atc act ccg   96
Ser Glu Lys Gly Glu Asp Met Lys Val Gly Tyr Asp Pro Ile Thr Pro
            20                  25                  30

cag aag gag gag ggt gcc tgg ttt ggg atc tgc agg gat gga agg ctg   144
Gln Lys Glu Glu Gly Ala Trp Phe Gly Ile Cys Arg Asp Gly Arg Leu
        35                  40                  45

ctg gct gct acc ctc ctg ctg gcc ctg ttg tcc agc agt ttc aca gcg   192
Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Ser Ser Phe Thr Ala
    50                  55                  60

atg tcc ttg tac cag ttg gct gcc ttg caa gca gac ctg atg aac ctg   240
Met Ser Leu Tyr Gln Leu Ala Ala Leu Gln Ala Asp Leu Met Asn Leu
 65                  70                  75                  80
```

```
cgc atg gag ctg cag agc tac cga ggt tca gca aca cca gcc gcc gcg   288
Arg Met Glu Leu Gln Ser Tyr Arg Gly Ser Ala Thr Pro Ala Ala Ala
                85                  90                  95

ggt gct cca gag ttg acc gct gga gtc aaa ctc ctg acg ccg gca gct   336
Gly Ala Pro Glu Leu Thr Ala Gly Val Lys Leu Leu Thr Pro Ala Ala
            100                 105                 110

cct cga ccc cac aac tcc agc cgc ggc cac agg aac aga cgc gct ttc   384
Pro Arg Pro His Asn Ser Ser Arg Gly His Arg Asn Arg Arg Ala Phe
        115                 120                 125

cag gga cca gag gaa aca gaa caa gat gta gac ctc tca gct cct cct   432
Gln Gly Pro Glu Glu Thr Glu Gln Asp Val Asp Leu Ser Ala Pro Pro
    130                 135                 140

gca cca tgc ctg cct gga tgc cgc cat tct caa cat gat gat aat gga   480
Ala Pro Cys Leu Pro Gly Cys Arg His Ser Gln His Asp Asp Asn Gly
145                 150                 155                 160

atg aac ctc aga aac atc att caa gac tgt ctg cag ctg att gca gac   528
Met Asn Leu Arg Asn Ile Ile Gln Asp Cys Leu Gln Leu Ile Ala Asp
                165                 170                 175

agc gac acg ccg act ata cga aaa gga act tac aca ttt gtt cca tgg   576
Ser Asp Thr Pro Thr Ile Arg Lys Gly Thr Tyr Thr Phe Val Pro Trp
            180                 185                 190

ctt ctc agc ttt aaa aga gga aat gcc ttg gag gag aaa gag aac aaa   624
Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu Glu Glu Lys Glu Asn Lys
        195                 200                 205

ata gtg gtg agg caa aca ggc tat ttc ttc atc tac agc cag gtt cta   672
Ile Val Val Arg Gln Thr Gly Tyr Phe Phe Ile Tyr Ser Gln Val Leu
    210                 215                 220

tac acg gac ccc atc ttt gct atg ggt cat gtc atc cag agg aag aaa   720
Tyr Thr Asp Pro Ile Phe Ala Met Gly His Val Ile Gln Arg Lys Lys
225                 230                 235                 240

gta cac gtc ttt ggg gac gag ctg agc ctg gtg acc ctg ttc cga tgt   768
Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys
                245                 250                 255

att cag aat atg ccc aaa aca ctg ccc aac aat tcc tgc tac tcg gct   816
Ile Gln Asn Met Pro Lys Thr Leu Pro Asn Asn Ser Cys Tyr Ser Ala
            260                 265                 270

ggc atc gcg agg ctg gaa gaa gga gat gag att cag ctt gca att cct   864
Gly Ile Ala Arg Leu Glu Glu Gly Asp Glu Ile Gln Leu Ala Ile Pro
        275                 280                 285

cgg gag aat gca cag att tca cgc aac gga gac gac acc ttc ttt ggt   912
Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly Asp Asp Thr Phe Phe Gly
    290                 295                 300

gcc cta aaa ctg ctg taa                                          930
Ala Leu Lys Leu Leu
305
```